REMARKS

Claims 1-17 are pending in this application. Claims 1-17 have been amended to distinctively claim the invented subject matter. The amendments are supported by the originally filed application. No new matter has been added.

Claims 1-7 and 13-17 have been rejected under 35 U.S.C. 112, second paragraph, as being indefinite

The Examiner rejects Claims 1-7 and 13-17 under 35 U.S.C. 112, second paragraph, as being indefinite. More specifically, the Examiner alleges that the "adapted to" (claims 1, 3, and 6) and "means" (claims 13-17) are not clear.

Applicant strongly believes that these two terms are not indefinite because they are commonly used in the patents relevant to computer/software inventions. Nonetheless, for the sake of expediting the examination process, these two terms have been deleted from the claims. Therefore, applicant respectfully requests that the rejections under 35 U.S.C. 112, second paragraph, be withdrawn.

Claims 1-17 have been rejected under 35 U.S.C. 101 as being directed to non-statutory subject matter

The Examiner rejects Claims 1-17 under 35 U.S.C. 101 as being non-statutory subject matter. More specifically, the Examiner alleges that Claims 1-17 are directed to software per se and the claimed invention lacks credible utility.

Applicant strongly disagrees with the characterization of the claimed invention by the Examiner. Nonetheless, applicant has amended claims 1-17. More specifically, claim 1 has been amended to claims "rostering computing system". In addition, the "computer usable medium" has been amended to "computer storage medium" as suggested by the Examiner. Therefore, Applicant respectfully submits that the rejections to claims 1-17 under 35 U.S.C. 101 be withdrawn.

As for the utility of the present invention, applicant respectfully submits that the present invention has the requisite utility for a patentable invention. It is true that GA is search heuristic that does not guarantee a global optimum. However, the claimed invention of the present application is not directed to an abstract GA software. Instead, Claims 1-17 are directed to a system/method that is based on GA to derive desirable solution for rosters. Rosters are practically important in many organizations including schools and hospitals where many resources including staff have to be allocated according to predetermined conditions. Therefore, a rostering computing system/method is useful.

Claims 1-17 have been rejected under 35 U.S.C. 102 as being anticipated by Boyd

The Examiner rejects Claims 1-17 under 35 U.S.C. 102 as being anticipated by Boyd. More specifically, the Examiner alleges that Boyd discloses all claimed elements in Claims 1-17 of the present application. After careful reading of Boyd, Applicant respectfully submits that the allegation is not supported by Boyd and thus Claims 1-17 are not anticipated by Boyd for the following reasons.

1. Boyd

Boyd discloses a **direct gene modeling method that is traditional and static.** The Figure R1 below illustrates the direct gene modeling method used by Boyd. Data used therein is copied from Boyd's Fig.1.
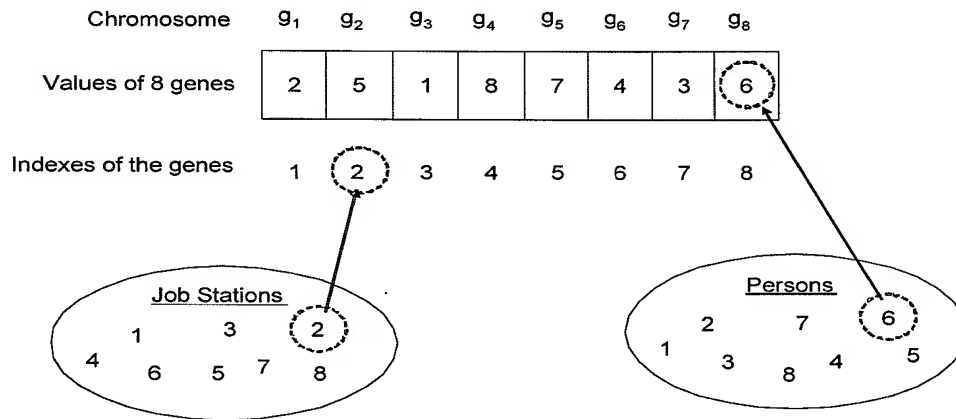
Boyd et al's Static Gene Modelling Method

Figure R1. Boyd's Static Gene Modelling Method

According to Boyd et al's direct gene coding method, the position (index) of a gene in a chromosome represents the job station (or job). There are 8 genes (g_1, g_2, ..., g_8) in a chromosome as shown in the Figure R1. The numbered gene at a location represents the person assigned to that job station. For example, Person numbered 6 is assigned to Job Station 8, as shown in FIG R1. According to Boyd's report, the number of genes in a chromosome is 16; each gene may take a value from the range from 1 to 24.

Boyd's method is a typically traditional direct coding and static gene modelling method, in which each gene in a chromosome directly represents one solution element. If there are N elements in a schedule solution (or chromosome), the GA system must utilize N genes in a chromosome, where the N is also called length of the chromosome (denoted as L_c).

It is well known in AI community that a preliminary condition that leads to a successful application of genetic algorithms is that solution space if the problem being addressed must be encoded using chromosomes with a manageable length, say typically, $L_c = 100$, e.g., a chromosome has 100 genes, or at most a few hundred genes. Current GA systems have great difficulty to perform evolution with lengthy chromosomes, for example, $L_c >= 500$.

Boyd's direct and static gene modelling method is not able to solve large and complex rostering problems because the length of the chromosome defined by the model is not manageable. Detailed explanation is given as follows.
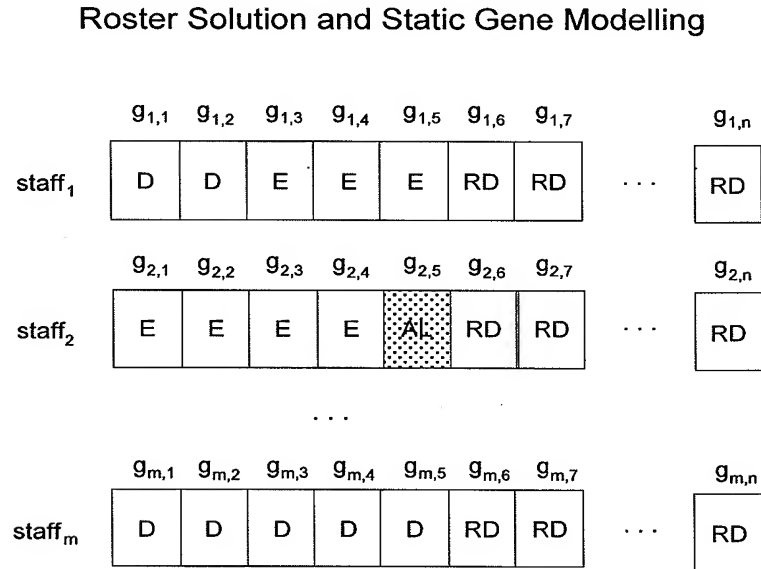
Roster Solution and Static Gene Modelling

$g_{1,1}$	$g_{1,2}$	$g_{1,3}$	$g_{1,4}$	$g_{1,5}$	$g_{1,6}$	$g_{1,7}$		$g_{1,n}$
D	D	E	E	E	RD	RD	···	RD

staff$_1$

$g_{2,1}$	$g_{2,2}$	$g_{2,3}$	$g_{2,4}$	$g_{2,5}$	$g_{2,6}$	$g_{2,7}$		$g_{2,n}$
E	E	E	E	AL	RD	RD	···	RD

staff$_2$

. . .

$g_{m,1}$	$g_{m,2}$	$g_{m,3}$	$g_{m,4}$	$g_{m,5}$	$g_{m,6}$	$g_{m,7}$		$g_{m,n}$
D	D	D	D	D	RD	RD	···	RD

staff$_m$

Figure R2. Roster Solution and Static Gene Modelling

Figure R2 shows a typical duty roster in form of an m×n two dimensional matrix. There are m staff are to be rostered during a period of n days. In a typical hospital nurse rostering problem, there are about one hundred nursing staff, the rostering period is typically 2 weeks (14 days) or 4 weeks (28 days). In Figure R2, D stands for day shift, E afternoon shift, RD rest day, AL annual leave. Note that AL in the figure is shaded which is fixed and not adjustable. If we use Boyd 's direct and static gene modelling method, the chromosome being used to encode the roster solution space must have m×n genes, e.g. , $L_c = 100 \times 14 = 1400$, or , $L_c = 100 \times 28 = 2800$ genes. Any one in the art should know that such GA systems definitely fail to search for a solution for a problem encoded using chromosomes that have 1400 or 2800 genes.

2. The claimed invention of the present application

Claims 1-17 are directed to rostering computing systems and methods represented by Claim 1. More specifically, the rostering computing system of Claim 1 is based on GA where the GA is operated on an initial shift list matrix that makes the rostering of the present invention indirect and dynamic, thus it overcomes the limitations of traditional direct gene modelling methods represented by Boyd's teachings. Therefore, the new method and system significantly reduce the length of chromosomes and improve GA technology so that it is possible to use GA systems to solve large and complex rostering problems.

Dynamic Gene Modelling Method Used in GA   Rostering

Indexes of the genes time unit (1 to n day)	1	2	3	4	5	6	7	Chromosome gene	Gene value
Initial shift list for staff $_1$	D	D	E	E	E	RD	RD	g_1	1
Initial shift list for staff $_2$	E	E	E	E	A	RD	RD	g_2	6
				...				:	
Initial shift list for staff$_m$	D	D	D	D	D	RD	RD	g_m	3

Figure R3. Rostering Gene Modelling with Shifting Factors

Unlike Boyd's traditional direct coding and gene modelling method, the gene in the chromosome of the claimed indirect coding or dynamic gene modelling method of the present application does not directly represent any element of the solution, e.g., gene does not represent any shift in the shift list. Instead, genes in a chromosome stores the information of how the initial shift lists are dynamically adjusted in order to achieve overall shift balance and to better satisfy constraints imposed. As shown in the Figure

R3, each staff is assigned with an initial shift list which contains shift loading (no of D shifts, no. of E shifts, and so on), rest days and leaves applied, etc. Note that the initial shift lists are not roster solution; and the sequence of the shifts in the initial shift list are not significant as they will be adjusted during the GA evolution in order to achieve required shift balance and to satisfy constraints imposed by the planners.

With this indirect coding method, a chromosome has m genes corresponding to m staff in the rostering problem, such as for example, 100 genes for a typical hospital ward with 100 nursing staff. It is noted that the length of the chromosome, where, $Lc = m$, defined using this new method is (n-1) times shorter than Boyd et al's method, Boyd et al's method defined a chromosome with m * n genes, e.g., $Lc = m * n$, where n is rostering period in terms of days.

To make the drawing more readable, we set the rostering period $n = 7$ days.

Each gene $(g1, g2, ..., g7)$ in the chromosome is a shifting factor that is associated with each of the initial shift list that is assigned to a staff. Each gene or shifting factor may take a value within a range from 1 to 7; the gene value represents the shifting position for that shift list. The shifting operation is illustrated in Figure R4.

As shown in Figure R4, $g_1 = 1$, the initial shift list assigned to $staff_1$ is not shifted at all; $g_2 = 6$, the initial shift list (E,E,E,E,AL, RD,RD) assigned to $staff_2$ is shifted from position 6, this shifting results in a new shift list "E,E,RD,RD, AL, E,E". Note that AL's position is not shifted because an approved leave is fixed on a particular date. Similarly, $g_n = 3$, the initial shift list (D,D,D,D,D, RD,RD) assigned to $staff_n$ is shifted from position 3, the shifting results in a new shift list "RD, RD, D,D,D,D". After shifting operation, the number of D and the number of E shifts per day are balanced, shown in the Figure R4. Of course, GA rostering system takes into account other optimization criteria when computing fitness of each chromosome to find fittest solutions.

Before shifting operation | After shifting operation

Day	1	2	3	4	5	6	7	Gene		1	2	3	4	5	6	7
$staff_1$	D	D	E	E	E	RD	RD	$g_1 = 1$		D	D	E	E	E	RD	RD
$staff_2$	E	E	E	E	AL	RD	RD	$g_2 = 6$		E	E	RD	RD	AL	E	E

...

| $staff_n$ | D | D | D | D | D | RD | RD | $g_n = 3$ | | RD | RD | D | D | D | D | D |

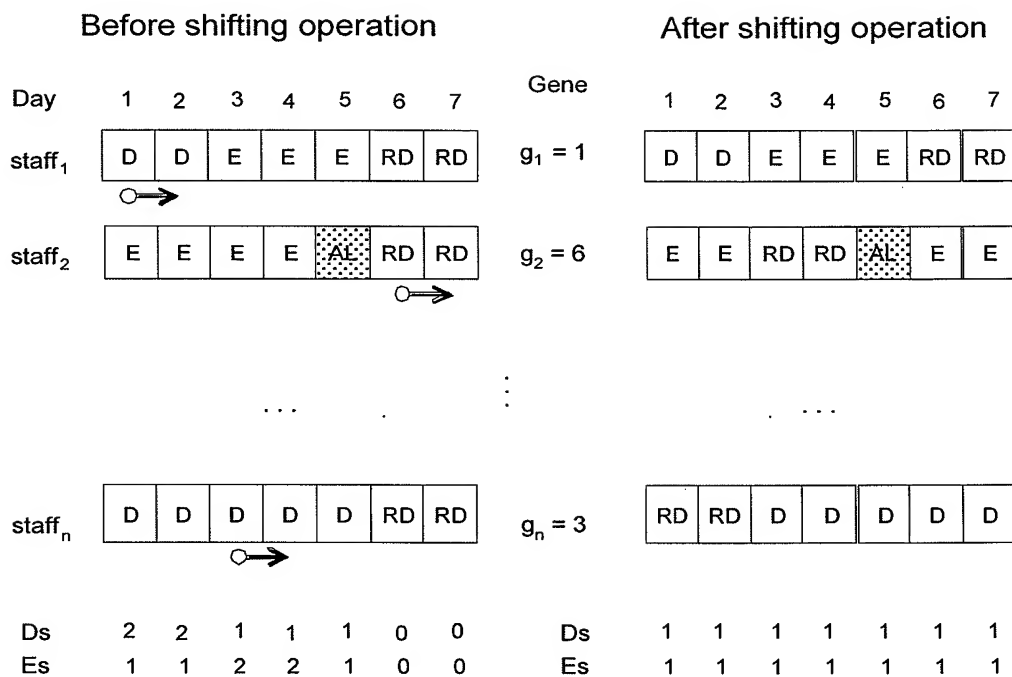| Ds | 2 | 2 | 1 | 1 | 1 | 0 | 0 | Ds | 1 | 1 | 1 | 1 | 1 | 1 | 1 |
| Es | 1 | 1 | 2 | 2 | 1 | 0 | 0 | Es | 1 | 1 | 1 | 1 | 1 | 1 | 1 |

Figure R4. Shift Lists Are Adjusted by Shifting Factors (Genes)

It is evident that the claimed rostering computing system and method of the present application is fundamentally different from the method taught by Boyd.

3. Conclusion

Claims 1-17 are not anticipated by Boyd because it fails to teach or suggest the rostering computing system and method based on GA using an initial shift list matrix.

Applicants respectfully request that a timely Notice of Allowance be issued in this case.

Respectfully submitted,

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